

T05511"25TE000T

1/9

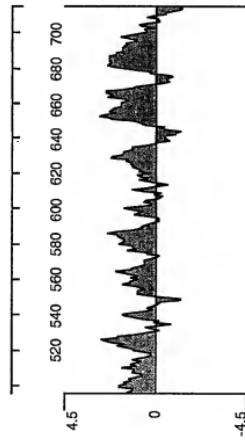
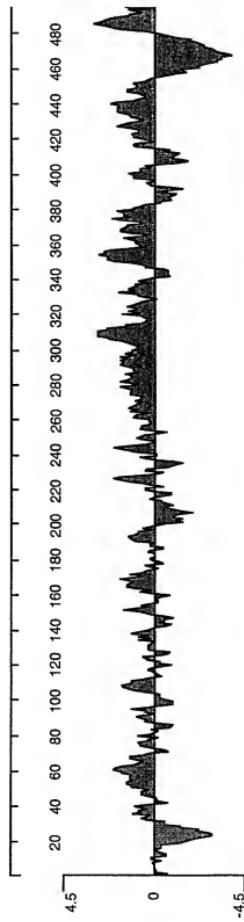


Fig. 1

ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
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 MGTAGG-----PSVIALIFAVCAPRLQAEGLDGCGHIVTSQDSCGTMITSKQYPCG  
 MYPGARGGGALARAAGRGLLALLAVASAPLRLQAEGLDGCGHIVTSQDSCGTMITSKQYPCG  
  
 ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
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 TPNYTCCEKILITPKGKRLLRLGDNIBKTCASDYLFLSSATDQGPGYCGSWAVPK  
  
 ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
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 ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
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 VAGDISGNVWDYGDYRTSLLCKAAIAHGLITDGLGHINLQSKGISHYBGLLNGVLSRH  
  
 ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
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 GSLSEKRFLPT-----  
 GSLSDRFLPT-----  
  
 ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
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 ZGI\_MUZCUB5X2\_3  
 ZGI\_MUZCUB5X3\_1  
 HUZCUB5X1\_2  
 IVNNEEKVFOQNSNFRDVQNNF1PPIVARYTRVVPOTWQRIALKVELGQITQNN

Fig. 2A

ZGL MUZCUB5X2_3	ZGL MUZCUB5X3_1										
HU7CUB5X1_2											
RKKKKNPVYSAACKTCWQKQKYPARRQESTEISYDNKEKNTQKDLITSDMADY		RKKKKNPVYSAACKTCWQKQKYPARRQESTEISYDNKEKNTQKDLITSDMADY		RKKKKNPVYSAACKTCWQKQKYPARRQESTEISYDNKEKNTQKDLITSDMADY		RKKKKNPVYSAACKTCWQKQKYPARRQESTEISYDNKEKNTQKDLITSDMADY		RKKKKNPVYSAACKTCWQKQKYPARRQESTEISYDNKEKNTQKDLITSDMADY		RKKKKNPVYSAACKTCWQKQKYPARRQESTEISYDNKEKNTQKDLITSDMADY	
ZGL MUZCUB5X2_3	ZGL MUZCUB5X3_1										
HU7CUB5X1_2											
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ZGL MUZCUB5X2_3	ZGL MUZCUB5X3_1										
HU7CUB5X1_2											
ATP1VERHLLRAHTPTOSGYVPGRPTKHSHSSGGFPPTA - TOVESYQRFASPKP		ATP1VERHLLRAHTPTOSGYVPGRPTKHSHSSGGFPPTA - TOVESYQRFASPKP		ATP1VERHLLRAHTPTOSGYVPGRPTKHSHSSGGFPPTA - TOVESYQRFASPKP		ATP1VERHLLRAHTPTOSGYVPGRPTKHSHSSGGFPPTA - TOVESYQRFASPKP		ATP1VERHLLRAHTPTOSGYVPGRPTKHSHSSGGFPPTA - TOVESYQRFASPKP		ATP1VERHLLRAHTPTOSGYVPGRPTKHSHSSGGFPPTA - TOVESYQRFASPKP	
ZGL MUZCUB5X2_3	ZGL MUZCUB5X3_1										
HU7CUB5X1_2											
VGGYDGPASSELSDERD - PASQSMTS - GEDDQSYSPRNLGLPLQMTMTALL		VGGYDGPASSELSDERD - PASQSMTS - GEDDQSYSPRNLGLPLQMTMTALL		VGGYDGPASSELSDERD - PASQSMTS - GEDDQSYSPRNLGLPLQMTMTALL		VGGYDGPASSELSDERD - PASQSMTS - GEDDQSYSPRNLGLPLQMTMTALL		VGGYDGPASSELSDERD - PASQSMTS - GEDDQSYSPRNLGLPLQMTMTALL		VGGYDGPASSELSDERD - PASQSMTS - GEDDQSYSPRNLGLPLQMTMTALL	
ZGL MUZCUB5X2_3	ZGL MUZCUB5X3_1										
HU7CUB5X1_2											
AGGTYDKEPASVSLAEDS - PAGSYOMTS - PRDCTPQPTGSDSYA - PRDCTPQMTMTALL		AGGTYDKEPASVSLAEDS - PAGSYOMTS - PRDCTPQPTGSDSYA - PRDCTPQMTMTALL		AGGTYDKEPASVSLAEDS - PAGSYOMTS - PRDCTPQPTGSDSYA - PRDCTPQMTMTALL		AGGTYDKEPASVSLAEDS - PAGSYOMTS - PRDCTPQPTGSDSYA - PRDCTPQMTMTALL		AGGTYDKEPASVSLAEDS - PAGSYOMTS - PRDCTPQPTGSDSYA - PRDCTPQMTMTALL		AGGTYDKEPASVSLAEDS - PAGSYOMTS - PRDCTPQPTGSDSYA - PRDCTPQMTMTALL	
ZGL MUZCUB5X2_3	ZGL MUZCUB5X3_1										
HU7CUB5X1_2											
(SSQ ID NO: 14)		(SSQ ID NO: 6)									

Fig. 2B

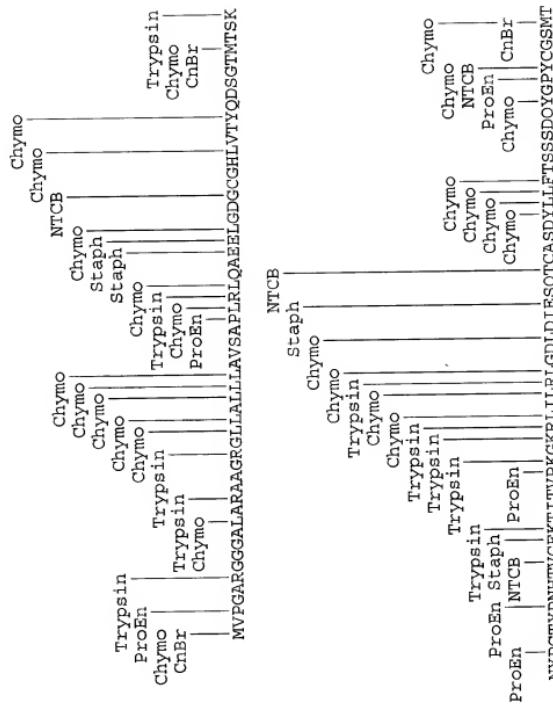


Fig. 3A

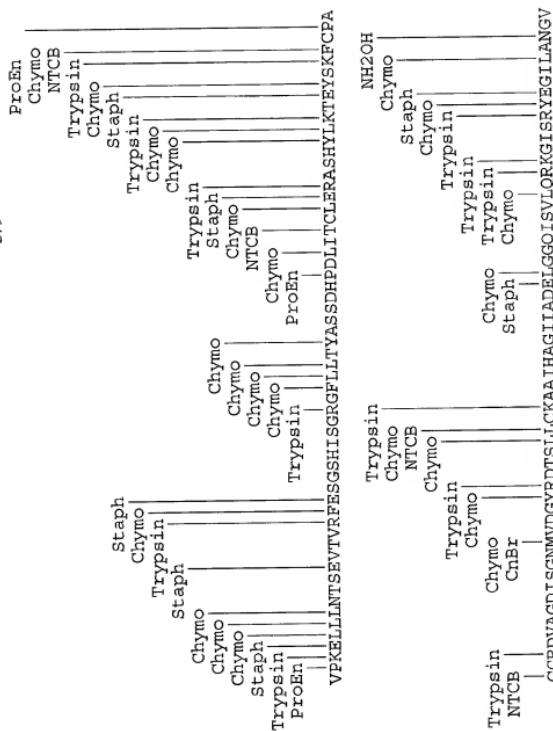


Fig. 3B

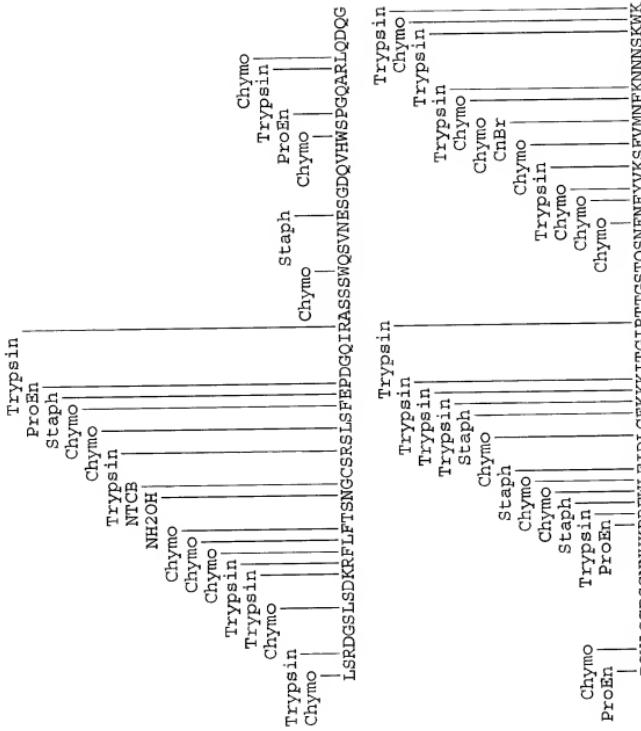


Fig. 3C

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7/9

NTCE

Diagram illustrating the proteolytic cleavage of the C-terminal region of human pro-IL-1 $\beta$  by various enzymes. The sequence is:

TYKGIVNNNEEKVFGNSNFRIIDFVQNNNFIPIPIVARYVRRVPPOTWHQRIALKVELIGQITQ

Cleavage sites are indicated by lines:

- Chymo (Chymotrypsin): Multiple sites throughout the sequence.
- Staph (Staphylococcal proteinase K): Multiple sites throughout the sequence.
- Trypsin: Multiple sites throughout the sequence.
- ProEn (Proteinase K): Multiple sites throughout the sequence.
- CnBr (Chloroform/magnesium bromide): Multiple sites throughout the sequence.

Fig. 3D

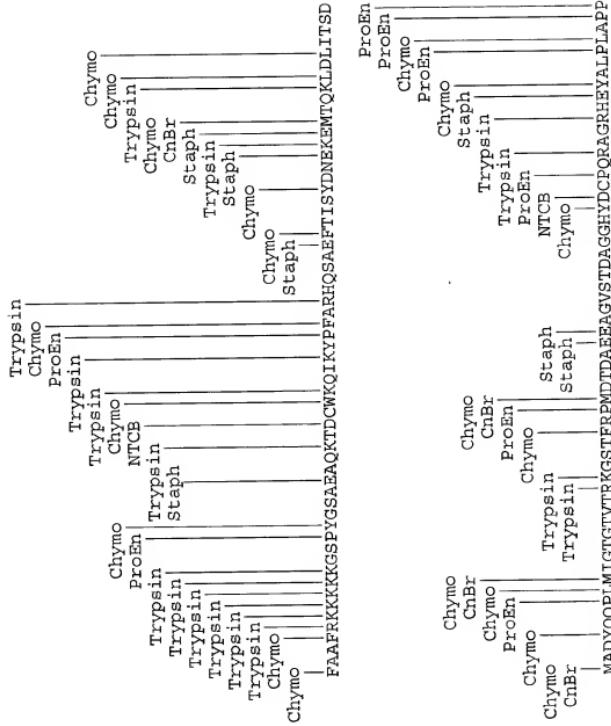


Fig. 3E

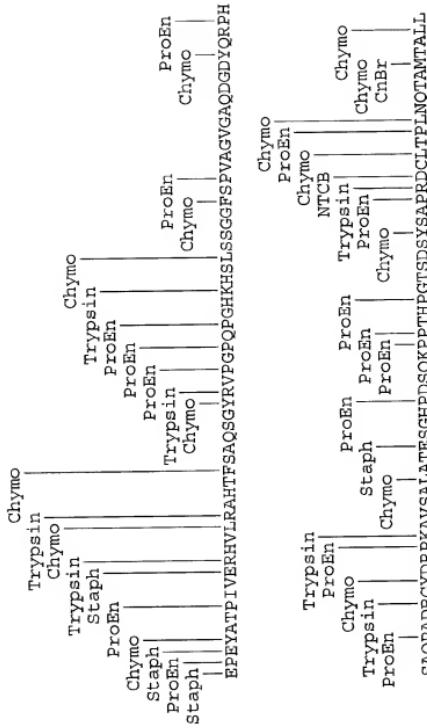


Fig. 3F